

**IN THE SPECIFICATION:**

Please replace the second full paragraph on page 8 with:

F<sub>1</sub> The  $\alpha$ - amylase structure is made up of three globular domains ordered A, B, and C with respect to sequence, which lie approximately along a line in the order B, A, C. The domains can be defined as being residues 1-103 and 206-395 for domain A, residues 104-205 for domain B, and residues 396-483 for domain C, the numbers referring to the *B. licheniformis*  $\alpha$ -amylase (SEQ ID NO:2). This gives rise to an elongated molecule, the longest axis being about 85 Å. The widest point perpendicular to this axis is approximately 50Å and spans the central A domain. The active site residues of the *B. licheniformis*  $\alpha$ -amylase (SEQ ID NO: 2) are D323, D231 and E261.

Please replace the fifth full paragraph on page 26 with:

F<sub>2</sub> The calcium site of Domain C of the *B. licheniformis*  $\alpha$ -amylase (SEQ ID NO: 2) may be stabilized by replacing the amino acid residues H408 and/or G303 with any other amino acid residue. Of particular interest is the following mutations: H408Q,E,N,D and/or G303N,D,Q,E which are contemplated to provide a better calcium binding or protection from calcium depletion.

ND 32  
Please replace the third full paragraph on page with:

NE  
Don't have  
page No.  
43  
Of particular interest is a variant of a Termamyl-like  $\alpha$ -amylase which comprises a mutation corresponding to one or more of the following mutations in the *B. licheniformis*  $\alpha$ -amylase (SEQ ID NO:2):

F350W

F343W

Please replace the sixth full paragraph on page 32 with:

F3 Of particular interest is a variant of a Termamyl-like  $\alpha$ -amylase which comprises a mutation corresponding to one or more of the following mutations in the *B. licheniformis*  $\alpha$ -amylase (SEQ ID NO:2):

L427F,L,W

V481,F,I,L,W

Please replace the third full paragraph to the fifth full paragraph on page 33:

F4 Especially interesting in this connection is deletion of three amino acids within the partial sequence from T369 to I377 (referring to the sequence of *B. licheniformis*  $\alpha$ -amylase; SEQ ID NO: 2), i.e. the partial sequence: T369-K370-G371-D372-S373-Q374-R375-E376-I377 (or the corresponding partial sequence in *B. amyloliquefaciens*  $\alpha$ -amylase; SEQ ID NO: 4). In addition to such deletions, substitution of one or more of the undeleted amino acids within the latter partial sequence may also be advantageous.

Preferable deletions of three amino acids in the partial sequence from T369 to I377 (in *B. licheniformis*  $\alpha$ -amylase; SEQ ID NO: 2) are deletion of K370+G371+D372 (i.e. K370\*+G371\*+D372\*) or deletion of D372+S373+Q374 (i.e. D372\*+S373\*+Q374\*) (or equivalent deletions in the corresponding partial sequence in *B. amyloliquefaciens*  $\alpha$ -amylase; SEQ ID NO: 4).